

Raw Sequence Listing Error Summary

| <u>ERROR DETECTED</u> | <u>SUGGESTED CORRECTION</u> | <u>SERIAL NUMBER:</u> <u>09/918,585</u> |
|---|---|---|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | | |
| 1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." | |
| 2 <input type="checkbox"/> Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. | |
| 3 <input type="checkbox"/> Misaligned Amino Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. | |
| 4 <input type="checkbox"/> Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. | |
| 5 <input type="checkbox"/> Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing. | |
| 6 <input type="checkbox"/> PatentIn 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences. | |
| 7 <input type="checkbox"/> Skipped Sequences (OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. | |
| 8 <input type="checkbox"/> Skipped Sequences (NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000 | |
| 9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 10 <input type="checkbox"/> Invalid <213> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence | |
| 11 <input checked="" type="checkbox"/> Use of <220> | Sequence(s) <u>157</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) | |
| 12 <input type="checkbox"/> PatentIn 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. | |
| 13 <input type="checkbox"/> Misuse of n | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide. | |

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/918,585

DATE: 08/10/2001
TIME: 07:58:44

Input Set : A:\GENENLAW-#94916-v1-Sequence_Listing_as_filed.WPD
Output Set: N:\CRF3\08102001\I918585.raw

3 <110> APPLICANT: Ashkenazi, Avi
4 Baker Kevin P.
5 Botstein, David
6 Desnoyers, Luc
7 Eaton, Dan
8 Ferrara, Napoleon
9 Filvaroff, Ellen
10 Fong, Sherman
11 Gao, Wei-Qiang
12 Gerber, Hanspeter
13 Gerritsen, Mary E.
14 Goddard, Audrey
15 Godowski, Paul J.
16 Grimaldi, J. Christopher
17 Gurney, Austin L.
18 Hillan, Kenneth J
19 Kljavin, Ivar J.
20 Kuo, Sophia S.
21 Napier, Mary A.
22 Pan, James;
23 Paoni, Nicholas F.
24 Roy, Margaret Ann
25 Shelton, David L.
26 Stewart, Timothy A.
27 Tumas, Daniel
28 Williams, P. Mickey
29 Wood, William I.

Does Not Comply
Corrected Diskette Needed

see page 6 of 8

31 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
32 Acids Encoding the Same

34 <130> FILE REFERENCE: P2630P1C1

C--> 36 <140> CURRENT APPLICATION NUMBER: US/09/918,585

C--> 36 <141> CURRENT FILING DATE: 2001-07-30

36 <150> PRIOR APPLICATION NUMBER: 60/062250

37 <151> PRIOR FILING DATE: 1997-10-17

39 <150> PRIOR APPLICATION NUMBER: 60/064249

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*improper format
not critical*

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<210> 157
<211> 412
<212> PRT
<213> Artificial

When field 213 is Artificial or Unknown
an explanation is required on fields 220
through fields 223.

<400> 157

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1 5 10 15

Gly Leu Leu Phe Leu Leu Leu Leu Met Leu Leu Ala Asp Pro
20 25 30

Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly
35 40 45

Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val
50 55 60

Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile
65 70 75

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/918,585

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TIME: 07:58:45

Input Set : A:\GENENLAW-\#94916-v1-Sequence_Listing_as_filed.WPD
Output Set: N:\CRF3\08102001\I918585.raw

L:36 M:270 C: Current Application Number differs, Replaced Current Application No
L:36 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:241 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:367 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:442 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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L:1038 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
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L:6386 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:6386 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: *Errored*
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L:7726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:8721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:10650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
L:10652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
L:10654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265